

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Kwon, Byoung Se
- (ii) TITLE OF INVENTION: New Receptor and Related Products and Methods
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Barnard, Brown & Michaels
 - (B) STREET: 306 East State Street, Suite 220
 - (C) CITY: Ithaca
 - (D) STATE: NY
 - (E) COUNTRY: USA
 - (F) ZIP: 14850
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: US
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- a4 (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: US 08/122,796
 - (B) FILING DATE: 13-SEP-1993
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: US 08/012,269
 - (B) FILING DATE: 01-FEB-1993
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: US 07/922,996
 - (B) FILING DATE: 30-JUL-1992
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: US 08/267,577
 - (B) FILING DATE: 07-NOV-1988
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Michaels, Christopher A
 - (B) REGISTRATION NUMBER: 34,390
 - (C) REFERENCE/DOCKET NUMBER: KWO4
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 607-273-1711
 - (B) TELEFAX: 607-273-2609

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 838 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: H4-1BB #1
- (D) DEVELOPMENTAL STAGE: Differentiated T-cell
- (G) CELL TYPE: Lymphocyte

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 41..805
- (D) OTHER INFORMATION: /codon_start= 41

/product= "H4-1BB"

/number= 1

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 41..802
- (D) OTHER INFORMATION: /codon_start= 41

/product= "H4-1BB"

/number= 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ay
ent.

AATCAGCTTT GCTAGTATCA TACCTGTGCC AGATTTCATC	ATG GGA AAC AGC TGT	55
	Met Gly Asn Ser Cys	
	1 5	
TAC AAC ATA GTA GCC ACT CTG TTG CTG GTC CTC AAC TTT GAG AGG ACA	103	
Tyr Asn Ile Val Ala Thr Leu Leu Leu Val Leu Asn Phe Glu Arg Thr		
10 15 20		
AGA TCA TTG CAG GAT CCT TGT AGT AAC TGC CCA GCT GGT ACA TTC TGT	151	
Arg Ser Leu Gln Asp Pro Cys Ser Asn Cys Pro Ala Gly Thr Phe Cys		
25 30 35		
GAT AAT AAC AGG AAT CAG ATT TGC AGT CCC TGT CCT CCA AAT AGT TTC	199	
Asp Asn Asn Arg Asn Gln Ile Cys Ser Pro Cys Pro Pro Asn Ser Phe		
40 45 50		
TCC AGC GCA GGT GGA CAA AGG ACC TGT GAC ATA TGC AGG CAG TGT AAA	247	
Ser Ser Ala Gly Gly Gln Arg Thr Cys Asp Ile Cys Arg Gln Cys Lys		
55 60 65		
GGT GTT TTC AGG ACC AGG AAG GAG TGT TCC TCC ACC AGC AAT GCA GAG	295	
Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser Thr Ser Asn Ala Glu		
70 75 80 85		
TGT GAC TGC ACT CCA GGG TTT CAC TGC CTG GGG GCA GGA TGC AGC ATG	343	
Cys Asp Cys Thr Pro Gly Phe His Cys Leu Gly Ala Gly Cys Ser Met		

90

95

100

TGT Cys	GAA Glu	CAG Gln	GAT Asp	TGT Cys	AAA Lys	CAA Gln	GGT Gly	CAA Gln	GAA Glu	CTG Leu	ACA Thr	AAA Lys	AAA Lys	GGT Gly	TGT Cys	391
			105					110						115		
AAA Lys	GAC Asp	TGT Cys	TGC Cys	TTT Phe	GGG Gly	ACA Thr	TTT Phe	AAC Asn	GAT Asp	CAG Gln	AAA Lys	CGT Arg	GGC Gly	ATC Ile	TGT Cys	439
		120					125					130				
CGA Arg	CCC Pro	TGG Trp	ACA Thr	AAC Asn	TGT Cys	TCT Ser	TTG Leu	GAT Asp	GGA Gly	AAG Lys	TCT Ser	GTG Val	CTT Leu	GTG Val	AAT Asn	487
	135					140					145					
GGG Gly	ACG Thr	AAG Lys	GAG Glu	AGG Arg	GAC Asp	GTG Val	GTC Val	TGT Cys	GGA Gly	CCA Pro	TCT Ser	CCA Pro	GCT Ala	GAC Asp	CTC Leu	535
150					155					160					165	
TCT Ser	CCG Pro	GGA Gly	GCA Ala	TCC Ser	TCT Ser	GTG Val	ACC Thr	CCG Pro	CCT Pro	GCC Ala	CCT Pro	GCG Ala	AGA Arg	GAG Glu	CCA Pro	583
				170					175					180		
GGA Gly	CAC His	TCT Ser	CCG Pro	CAG Gln	ATC Ile	ATC Ile	TCC Ser	TTC Phe	TTT Phe	CTT Leu	GCG Ala	CTG Leu	ACG Thr	TCG Ser	ACT Thr	631
			185					190					195			
GCG Ala	TTG Leu	CTC Leu	TTC Phe	CTG Leu	CTG Leu	TTC Phe	TTC Phe	CTC Leu	ACG Thr	CTC Leu	CGT Arg	TTC Phe	TCT Ser	GTT Val	GTT Val	679
		200					205					210				
AAA Lys	CGG Arg	GGC Gly	AGA Arg	AAG Lys	AAA Lys	CTC Leu	CTG Leu	TAT Tyr	ATA Ile	TTC Phe	AAA Lys	CAA Gln	CCA Pro	TTT Phe	ATG Met	727
	215					220					225					
AGA Arg	CCA Pro	GTA Val	CAA Gln	ACT Thr	ACT Thr	CAA Gln	GAG Glu	GAA Glu	GAT Asp	GGC Gly	TGT Cys	AGC Ser	TGC Cys	CGA Arg	TTT Phe	775
230					235					240					245	
CCA Pro	GAA Glu	GAA Glu	GAA Glu	GAA Glu	GGA Gly	GGA Gly	TGT Cys	GAA Glu	CTG Leu	TGAAATGGAA	GTCAATAGGG					825
				250					255							
CTGTTGGGAC	TTT															838

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Gly	Asn	Ser	Cys	Tyr	Asn	Ile	Val	Ala	Thr	Leu	Leu	Leu	Val	Leu	
1				5					10					15		
Asn	Phe	Glu	Arg	Thr	Arg	Ser	Leu	Gln	Asp	Pro	Cys	Ser	Asn	Cys	Pro	

20

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Ala Gly Thr Phe Cys Asp Asn Asn Arg Asn Gln Ile Cys Ser Pro Cys
35 40 45

Pro Pro Asn Ser Phe Ser Ser Ala Gly Gly Gln Arg Thr Cys Asp Ile
50 55 60

Cys Arg Gln Cys Lys Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser
65 70 75 80

Thr Ser Asn Ala Glu Cys Asp Cys Thr Pro Gly Phe His Cys Leu Gly
85 90 95

Ala Gly Cys Ser Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu
100 105 110

Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln
115 120 125

Lys Arg Gly Ile Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys
130 135 140

Ser Val Leu Val Asn Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro
145 150 155 160

Ser Pro Ala Asp Leu Ser Pro Gly Ala Ser Ser Val Thr Pro Pro Ala
165 170 175

Pro Ala Arg Glu Pro Gly His Ser Pro Gln Ile Ile Ser Phe Phe Leu
180 185 190

Ala Leu Thr Ser Thr Ala Leu Leu Phe Leu Leu Phe Phe Leu Thr Leu
195 200 205

Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
210 215 220

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
225 230 235 240

Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
245 250 255

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PCR Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTYTGYMGAA ARTAYAAAYCC

20

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTYTCSTSCA HTGGTGGACA

20

(2) INFORMATION FOR SEQ ID NO:5:

*at
ant.*

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCCARGSWRC AGGTYTTRCA

20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTYTGRTCRT TRAATGTTCC

20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

a4
unrel. (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATAAGCTTT GCTAGTATCA TACCT

25

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTAAGATCTC TGCGGAGAGT GTCCTGGCTC

30